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OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:30 ; Search time 66.75 Seconds

(without alignments)
37.620 Million cell updates/sec

Title: US-09-846-033B-36

Sequence: 1 DRSNLTR 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 7

Total number of hits satisfying chosen parameters: 158

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp19808:*
- 2: geneseqp19908:*
- 3: geneseqp20008:*
- 4: geneseqp20018:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20038:*
- 8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	7	4	AAB84241	AAB84241 Zinc prot
2	100.0	7	5	ABB80798	ABB80798 Human ER-
3	100.0	7	5	ABB80812	ABB80812 Human ER-
4	100.0	7	5	ABP50162	ABP50162 Zinc fmg
5	100.0	7	5	ABP50914	ABP50914 Zinc fmg
6	100.0	7	5	ABP51092	ABP51092 Zinc fmg
7	100.0	7	5	ABP50535	ABP50535 Zinc fmg
8	100.0	7	5	ABP49313	ABP49313 Zinc fmg
9	100.0	7	5	ABP50277	ABP50277 Zinc fmg
10	100.0	7	5	ABP50373	ABP50373 Zinc fmg
11	100.0	7	5	ABP48386	ABP48386 Zinc fmg
12	100.0	7	5	ABP49231	ABP49231 Zinc fmg
13	100.0	7	5	ABP49241	ABP49241 Zinc fmg
14	100.0	7	5	ABP49259	ABP49259 Zinc fmg
15	100.0	7	5	ABP49880	ABP49880 Zinc fmg
16	100.0	7	5	ABP50861	ABP50861 Zinc fmg
17	100.0	7	5	ABP50538	ABP50538 Zinc fmg
18	100.0	7	5	ABP50920	ABP50920 Zinc fmg
19	100.0	7	5	ABP50858	ABP50858 Zinc fmg
20	100.0	7	5	ABP49274	ABP49274 Zinc fmg
21	100.0	7	5	ABP50311	ABP50311 Zinc fmg
22	100.0	7	5	ABP51150	ABP51150 Zinc fmg
23	100.0	7	5	ABP49769	ABP49769 Zinc fmg
24	100.0	7	5	ABP51159	ABP51159 Zinc fmg
25	100.0	7	5	ABP51180	ABP51180 Zinc fmg

26	7	100.0	7	5	ABP49201	ABP49201 Zinc fmg
27	7	100.0	7	5	ABP49224	ABP49224 Zinc fmg
28	7	100.0	7	5	ABP49666	ABP49666 Zinc fmg
29	7	100.0	7	5	ABP49958	ABP49958 Zinc fmg
30	7	100.0	7	5	ABP50823	ABP50823 Zinc fmg
31	7	100.0	7	5	ABP51101	ABP51101 Zinc fmg
32	7	100.0	7	5	ABP51147	ABP51147 Zinc fmg
33	7	100.0	7	5	ABP49964	ABP49964 Zinc fmg
34	7	100.0	7	5	ABP50254	ABP50254 Zinc fmg
35	7	100.0	7	5	ABP50521	ABP50521 Zinc fmg
36	7	100.0	7	5	ABP50524	ABP50524 Zinc fmg
37	7	100.0	7	5	ABP50542	ABP50542 Zinc fmg
38	7	100.0	7	5	ABP50545	ABP50545 Zinc fmg
39	7	100.0	7	5	ABP50166	ABP50166 Zinc fmg
40	7	100.0	7	5	ABP49157	ABP49157 Zinc fmg
41	7	100.0	7	5	ABP50056	ABP50056 Zinc fmg
42	7	100.0	7	5	ABJ03824	ABJ03824 Human VEG
43	7	100.0	7	5	ABJ03812	ABJ03812 Human VEG
44	7	100.0	7	5	ABJ03888	ABJ03888 Human VEG
45	7	100.0	7	5	ABJ03910	ABJ03910 Human VEG

ALIGNMENTS

RESULT 1
AAB84241 standard; peptide, 7 AA.
XX
AC AAB84241;
DT 06-AUG-2001 (first entry)
DE Zinc protein recognition helix SB89 for target DNA triplet GAC.
XX Phenotype associated gene; zinc finger protein; cancer; nephritis;
KW prostate hypertrophy; hematopoiesis; osteoporosis; obesity;
KM cardiovascular disease; diabetes.
XX
OS Synthetic.
XX
PN WO200140798-A2.
XX
PD 07-JUN-2001.
XX
PF 06-DEC-2000; 2000WO-US033086.
XX
PR 06-DEC-1999; 99US-00456100.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Case CC, Liu Q, Rebar EJ;
XX
DR WPI; 2001-374953/39.
XX
PT Identifying genes associated with selected phenotype for research
PT purposes, involves culturing cells transduced with nucleic acid encoding
PT zinc finger proteins and assaying cells exhibiting selected phenotype.
XX
PS Example 1; Page 36; 58pp; English.
XX
CC The specification describes a method for identifying genes associated
CC with a selected phenotype. The method involves providing a library of
CC nucleotide sequences encoding partially randomized zinc finger proteins,
CC transducing cells with expression vectors, each comprising a sequence
CC from the library, culturing the cells for expressing the zinc finger
CC protein, assaying the cells for selected phenotype, and identifying the
CC gene of interest, in cells exhibiting the phenotype. The method is useful
CC for identifying a gene or genes associated with a selected phenotype such
CC as the one related to cancer, nephritis, prostate hypertrophy,
CC hemopoiesis, osteoporosis, obesity, cardiovascular disease or diabetes.
CC The method is useful in academic laboratories, in the biotechnological
CC industries, and in pharmaceutical, genomic, agricultural and chemical

CC companies. AAB84233-44 represent recognition helices of zinc finger
 CC proteins, which recognise different DNA triplets
 CC
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 7; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRSNLTTR 7
 Db 1 DRSNLTTR 7
 RESULT 2
 ABB80798
 ID ABB80798 standard; peptide; 7 AA.
 AC ABB80798;
 XX
 DT 23-SEP-2002 (first entry)
 XX Human ER-alpha locus targeting ZFP1 peptide #8.
 DE
 XX ZFP; cytostatic; antidiabetic; ophthalmological; vasotropic; chromatin;
 KW gene expression; antirheumatic; antiarthritic; antiporiatic; nocrotropic;
 KW neuroprotective; cerebroprotective; estrogen receptor alpha; ER-alpha;
 KW zinc finger protein.
 XX
 OS Synthetic.
 XX
 XX WO200244386-A2.
 PN
 XX
 PD 06-JUN-2002.
 XX
 XX 30-NOV-2001; 2001WO-US045098.
 PF
 XX
 XX 01-DEC-2000; 2000US-0250804P.
 PR
 XX
 XX (SANG-) SANGAMO BIOSCIENCES INC.
 PA
 XX
 XX Wolffe AP, Tse C, Collingwood T;
 XX
 XX WPI; 2002-537455/57.
 DR
 XX
 XX
 PT Regulating expression of gene by contacting cell with regulatory molecule
 PT comprising DNA-binding domain targeted to sequence within accessible
 PT region of cellular chromatin associated with a gene, and functional
 PT domain.
 PS
 XX Example 1; Page 44; 64pp; English.
 XX
 CC The invention relates to regulating the expression of a gene residing in
 CC the chromatin of a cell. The method involves identifying one or more
 CC accessible regions in cellular chromatin associated with gene; designing
 CC a regulatory molecule, where the regulatory molecule comprises a DNA-
 CC binding domain targeted to a sequence within the accessible region, and a
 CC functional domain; and contacting the regulatory molecule with the cell.
 CC The method is used for regulating the expression of a gene (e.g., a gene
 CC encoding a nuclear receptor such as estrogen receptor alpha (ERalpha),
 CC estrogen receptor beta (ERbeta), hepatocyte nuclear factor 4 alpha
 CC (HNF4alpha), hepatocyte nuclear factor 4 gamma (HNF4gamma), peroxisome
 CC proliferator activated receptor gamma (PPARGgamma), retinoid X receptor
 CC alpha (RXRalpha), or constitutively active receptor alpha (CARalpha))
 CC residing in the chromatin of a cell. Regulation of gene expression (such
 CC as nuclear receptor genes) will be useful in treatment of various
 CC diseases, including cancer, diabetes and cardiovascular disease, where
 CC the regulatory molecule as described above, is contacted with the cell to
 CC carry out the regulation. The method is also useful for modulation of
 CC gene expression for therapeutic or prophylactic applications e.g.,
 CC diabetic retinopathy, ischemia, macular degeneration, rheumatoid
 CC arthritis, psoriasis, HIV infection, sickle cell anemia, Alzheimer's
 CC disease, stroke, etc. The method also has applications in pharmaceutical

CC research of both nuclear receptors of known function as well as those of
 CC unknown function. The method also facilitates development of tissue and
 CC animal models of disease states; drug validation, and therapeutic product
 CC development. The methods also allow identification of the role of nuclear
 CC receptors of unknown functions in cellular homeostasis. Sequences
 CC ABB80791-817 represent zinc finger protein (ZFP) DNA-binding domains that
 CC were fused to functional domains and tested for their ability to regulate
 CC expression of the ER in living cells
 CC
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 7; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRSNLTTR 7
 Db 1 DRSNLTTR 7
 RESULT 3
 ABB80812
 ID ABB80812 standard; peptide; 7 AA.
 AC ABB80812;
 XX
 DT 23-SEP-2002 (first entry)
 XX Human ER-alpha locus targeting ZFP3 peptide #4.
 DE
 XX ZFP; cytostatic; antidiabetic; ophthalmological; vasotropic; chromatin;
 KW gene expression; antirheumatic; antiarthritic; antiporiatic; nocrotropic;
 KW neuroprotective; cerebroprotective; estrogen receptor alpha; ER-alpha;
 KW zinc finger protein.
 XX
 OS Synthetic.
 XX
 XX WO200244386-A2.
 PN
 XX
 PD 06-JUN-2002.
 XX
 XX 30-NOV-2001; 2001WO-US045098.
 PF
 XX
 XX 01-DEC-2000; 2000US-0250804P.
 PR
 XX
 XX (SANG-) SANGAMO BIOSCIENCES INC.
 PA
 XX
 XX Wolffe AP, Tse C, Collingwood T;
 XX
 XX WPI; 2002-537455/57.
 DR
 XX
 XX
 PT Regulating expression of gene by contacting cell with regulatory molecule
 PT comprising DNA-binding domain targeted to sequence within accessible
 PT region of cellular chromatin associated with a gene, and functional
 PT domain.
 PS
 XX Example 1; Page 44; 64pp; English.
 XX
 CC The invention relates to regulating the expression of a gene residing in
 CC the chromatin of a cell. The method involves identifying one or more
 CC accessible regions in cellular chromatin associated with gene; designing
 CC a regulatory molecule, where the regulatory molecule comprises a DNA-
 CC binding domain targeted to a sequence within the accessible region, and a
 CC functional domain; and contacting the regulatory molecule with the cell.
 CC The method is used for regulating the expression of a gene (e.g., a gene
 CC encoding a nuclear receptor such as estrogen receptor alpha (ERalpha),
 CC estrogen receptor beta (ERbeta), hepatocyte nuclear factor 4 alpha
 CC (HNF4alpha), hepatocyte nuclear factor 4 gamma (HNF4gamma), peroxisome
 CC proliferator activated receptor gamma (PPARGgamma), retinoid X receptor
 CC alpha (RXRalpha), or constitutively active receptor alpha (CARalpha))
 CC residing in the chromatin of a cell. Regulation of gene expression (such
 CC as nuclear receptor genes) will be useful in treatment of various
 CC diseases, including cancer, diabetes and cardiovascular disease, where

CC the regulatory molecule as described above, is contacted with the cell to
CC carry out the regulation. The method is also useful for modulation of
CC gene expression for therapeutic or prophylactic applications e.g.,
CC diabetic retinopathy, ischaemia, macular degeneration, rheumatoid
CC arthritis, psoriasis, HIV infection, sickle cell anemia, Alzheimer's
CC disease, stroke, etc. The method also has applications in pharmaceutical
CC research of both nuclear receptors of known function as well as those of
CC unknown function. The method also facilitates development of tissue and
CC animal models of disease states, drug validation, and therapeutic product
CC development. The methods also allow identification of the role of nuclear
CC receptors of unknown functions in cellular homeostasis. Sequences
CC AB880791-817 represent zinc finger protein (ZFP) DNA-binding domains that
CC were fused to functional domains and tested for their ability to regulate
CC expression of the ER in living cells

XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTNR 7
|||
Db 1 DRSNLTNR 7

RESULT 4
ABP50162
ID ABP50162 standard; peptide; 7 AA.

XX AC ABP50162;

XX DT 28-AUG-2002 (first entry)

XX DE Zinc finger protein related peptide motif SEQ ID NO:3666.

XX KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200242459-A2.

XX PD 30-MAY-2002.

XX PF 20-NOV-2001; 2001WO-US043438.

XX PR 20-NOV-2000; 2000US-00716637.

XX PA (SANG-) SANGAMO BIOSCIENCES INC.

XX PI Liu Q;

XX DR WPI; 2002-500284/53.

XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.

XX PS Example 1; Page 57; 81pp; English.

XX
CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (1) involves selecting the F1 zinc finger such that it
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such
CC that it binds to the S3 target sub-site, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target sub-sites
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is

CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (II) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention

XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTNR 7
|||
Db 1 DRSNLTNR 7

RESULT 5
ABP50914
ID ABP50914 standard; peptide; 7 AA.

XX AC ABP50914;

XX DT 28-AUG-2002 (first entry)

XX DE Zinc finger protein related peptide motif SEQ ID NO:3417.

XX KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200242459-A2.

XX PD 30-MAY-2002.

XX PF 20-NOV-2001; 2001WO-US043438.

XX PR 20-NOV-2000; 2000US-00716637.

XX PA (SANG-) SANGAMO BIOSCIENCES INC.

XX PI Liu Q;

XX DR WPI; 2002-500284/53.

XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.

XX PS Example 1; Page 62; 81pp; English.

XX
CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (1) involves selecting the F1 zinc finger such that it
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such
CC that it binds to the S3 target sub-site, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target sub-sites
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid

CC in a sample, and in assays to determined the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTR 7
 |||||
 Db 1 DRSNLTR 7

RESULT 6
 ABP51092

ID ABP51092 standard; peptide; 7 AA.

AC ABP51092;

XX 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:3976.

KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX Homo sapiens.

OS Synthetic.

PN WO200242459-A2.

XX 30-MAY-2002.

XX 20-NOV-2001; 2001MO-US043438.

XX 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

XX WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying
 PT gene function and for human therapeutics and plant engineering, comprises
 PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 63; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target sub-site. Also described are: (1) a polypeptide
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it
 CC binds to the S2 target sub-site, and selecting the F3 zinc finger such
 CC that it binds to the S3 target sub-site, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target sub-sites
 CC having the nucleotide G in the 5'-most position of the sub-site. (I) is
 CC useful in studying gene function, and for human therapeutics and plant
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determined the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc

CC finger peptides which are given in the exemplification of the present
 CC invention

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTR 7
 |||||
 Db 1 DRSNLTR 7

RESULT 7
 ABP50535

ID ABP50535 standard; peptide; 7 AA.

AC ABP50535;

XX 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:2791.

KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX Homo sapiens.

OS Synthetic.

PN WO200242459-A2.

XX 30-MAY-2002.

XX 20-NOV-2001; 2001MO-US043438.

XX 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

XX WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying
 PT gene function and for human therapeutics and plant engineering, comprises
 PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 59; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target sub-site. Also described are: (1) a polypeptide
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it
 CC binds to the S2 target sub-site, and selecting the F3 zinc finger such
 CC that it binds to the S3 target sub-site, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target sub-sites
 CC having the nucleotide G in the 5'-most position of the sub-site. (I) is
 CC useful in studying gene function, and for human therapeutics and plant
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determined the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRSNLTTR 7
Db 1 DRSNLTTR 7

RESULT 8
ABP49313
ID ABP49313 standard; peptide; 7 AA.

AC ABP49313;
XX 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:1577.

XX Zinc finger protein; ZFP; DNA binding protein; zinc finger.

OS Homo sapiens.
XX Synthetic.

PN W0200242459-A2.

PD 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US043438.

PR 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

XX Liu Q;

XX WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.

XX Example 1; Page 48; 81pp; English.

CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide
CC (I1) comprising (I); (2) a polynucleotide (I11) encoding (I) or (I1); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such
CC that it binds to the S3 target sub-site, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target sub-sites
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I1), (I1) or (I11) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject. In
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I1) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. AB071213 to
CC AB072214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRSNLTTR 7
Db 1 DRSNLTTR 7

RESULT 9
ABP50277
ID ABP50277 standard; peptide; 7 AA.

AC ABP50277;

XX 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:2705.

XX Zinc finger protein; ZFP; DNA binding protein; zinc finger.

OS Homo sapiens.
XX Synthetic.

PN W0200242459-A2.

PD 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US043438.

PR 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

XX Liu Q;

XX WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.

XX Example 1; Page 57; 81pp; English.

CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide
CC (I1) comprising (I); (2) a polynucleotide (I11) encoding (I) or (I1); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such
CC that it binds to the S3 target sub-site, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target sub-sites
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I1), (I1) or (I11) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject. In
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I1) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. AB071213 to
CC AB072214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
ABP50373
ID ABP50373 standard; peptide; 7 AA.
XX
AC ABP50373;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related peptide motif SEQ ID NO:2737.
XX
KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX
OS Homo sapiens.
XX Synthetic.
XX WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US043438.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
LIU Q;
XX WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS Example 1; Page 58; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such
CC that it binds to the S3 target sub-site, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target sub-sites
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRSNLTR 7
| | | | |
DB 1 DRSNLTR 7
RESULT 11
ABP48386

ID ABP48386 standard; peptide; 7 AA.
XX
AC ABP48386;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related peptide motif SEQ ID NO:395.
XX
KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX
OS Homo sapiens.
XX Synthetic.
XX WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US043438.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
LIU Q;
XX WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS Example 1; Page 37; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such
CC that it binds to the S3 target sub-site, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target sub-sites
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRSNLTR 7
| | | | |
DB 1 DRSNLTR 7
RESULT 12
ABP49231
ID ABP49231 standard; peptide; 7 AA.
XX
AC ABP49231;
XX


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XX MO200242459-A2.
PN
XX
XX 30-MAY-2002.
PD
XX
XX 20-NOV-2001; 2001WO-US043438.
PF
XX 20-NOV-2000; 2000US-00716637.
PR
XX 20-NOV-2000; 2000US-00716637.
XX
XX (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX Liu Q;
XX
XX WPI; 2002-500284/53.
XX
XX
XX New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX
XX Example 1; Page 48; 81bp; English.
XX
XX The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target sub-site. Also described are: (i) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such
CC that it binds to the S3 target sub-site, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target sub-sites
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
CC
XX
XX Sequence 7 AA;
SQ
Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRSNLTTR 7
DB 1 DRSNLTTR 7
RESULT 15
ABP49880
ID ABP49880 standard; peptide: 7 AA.
XX
XX ABP49880;
AC
XX
XX 28-AUG-2002 (first entry)
DT
XX
XX Zinc finger protein related peptide motif SEQ ID NO:3572.
DE
XX
XX Zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX MO200242459-A2.
XX
XX PN
XX 30-MAY-2002.
PD
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XX
XX 20-NOV-2001; 2001WO-US043438.
PF
XX
XX 20-NOV-2000; 2000US-00716637.
PR
XX
XX (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX Liu Q;
XX
XX WPI; 2002-500284/53.
XX
XX
XX New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX
XX Example 1; Page 55; 81bp; English.
XX
XX The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target sub-site. Also described are: (i) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such
CC that it binds to the S3 target sub-site, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target sub-sites
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
CC
XX
XX Sequence 7 AA;
SQ
Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRSNLTTR 7
DB 1 DRSNLTTR 7
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Search completed: December 27, 2004, 18:06:44
Job time : 67.75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:31 ; Search time 15.8 Seconds
(without alignments)
29.381 Million cell updates/sec

Title: US-09-846-033B-36

Perfect score: 7

Sequence: 1 DRSNLTR 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 4 summaries

Database : Issued Patents AA.*

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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-731-558-20
2	7	100.0	27	4	US-09-424-487B-11
3	7	100.0	89	3	US-08-793-408-18
4	7	100.0	89	3	US-09-139-762A-18

ALIGNMENTS

RESULT 1
US-09-731-558-20
; Sequence 20, Application US/09731558
; Patent No. 6503717
; GENERAL INFORMATION:
; APPLICANT: Casey Christopher
; APPLICANT: Liu, Qiang
; APPLICANT: Redar, Edward J.
; APPLICANT: Sangam Biosciences, Inc.
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
; FILE REFERENCE: 019496-003210US
; CURRENT APPLICATION NUMBER: US/09/731,558
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 09/456,100
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SB59
; OTHER INFORMATION: recognition helix
US-09-731-558-20

Query Match 100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTR 7
|||
Db 1 DRSNLTR 7

RESULT 2

US-09-424-487B-11

; Sequence 11, Application US/09424487B

; Patent No. 6746838

; GENERAL INFORMATION:

; APPLICANT: CHOO, YEN

; APPLICANT: KLUG, AARON

; APPLICANT: ISALAN, MARK

; TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS

; FILE REFERENCE: 71278/264975

; CURRENT APPLICATION NUMBER: US/09/424,487B

; CURRENT FILING DATE: 2000-02-29

; PRIOR APPLICATION NUMBER: GB 9710809.6

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: PCT/GB98/01512

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 27

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger

; OTHER INFORMATION: peptide

US-09-424-487B-11

Query Match

Best Local Similarity 100.0%; Score 7; DB 4; Length 27;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTR 7
|||
Db 12 DRSNLTR 18

RESULT 3

US-08-793-408-18

; Sequence 18, Application US/08793408

; Patent No. 6007988

; GENERAL INFORMATION:

; APPLICANT: Choo, Yen

; APPLICANT: Klug, Aaron

; APPLICANT: Sanchez Garcia, Isidro

; TITLE OF INVENTION: Improvements in or Relating to

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESS: Pillsbury Madison & Sutro, L.L.P.

; STREET: 1100 New York Avenue, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3918

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,408
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-793-408-18

Query Match      100.0%; Score 7; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 DRSNLTTR 7
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Db      74 DRSNLTTR 80
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RESULT 4
US-09-139-762A-18
; Sequence 18, Application US/09139762A
; Patent No. 6013453
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Sanchez Garcia, Isidro
; TITLE OF INVENTION: Improvements in or Relating to
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-139-762A-18
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Query Match      100.0%; Score 7; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 DRSNLTTR 7
        |||||
Db      74 DRSNLTTR 80
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Search completed: December 27, 2004, 18:12:04
job time : 16.8 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:31 ; Search time 15.8 Seconds
(without alignments)
29.381 Million cell updates/sec

Title: US-09-846-033b-35
Perfect score: 7
Sequence: 1 RSDNLAR 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4 US-09-731-558-13	Sequence 13, Appl
2	7	100.0	7	4 US-09-779-233-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-731-558-13
; Sequence 13, Application US/09731558
; Patent No. 6503717
; GENERAL INFORMATION:
; APPLICANT: Casey, Casey Christopher
; APPLICANT: Liu, Qiang
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
; FILE REFERENCE: 019496-003210US
; CURRENT APPLICATION NUMBER: US/09/731,558
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 09/456,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 7

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SB52
US-09-731-558-13

Query Match 100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDNLAR 7
Db 1 RSDNLAR 7

RESULT 2
US-09-779-233-43
; Sequence 43, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Casey, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recognition
US-09-779-233-43

Query Match 100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDNLAR 7
Db 1 RSDNLAR 7

Search completed: December 27, 2004, 18:12:03
Job time : 15.8 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:30 : Search time 66.75 Seconds
(without alignments)
37.620 Million cell updates/sec

Title: US-09-846-033B-34

Perfect score: 7

Sequence: 1 RSDHLAR 7

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 35872929 residues

Word size : 7

Total number of hits satisfying chosen parameters: 165

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A.GeneSeq.23Sep04:*

1: _ geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	7	100.0	7	5 ABB80792	ABB80792 Human ER-
3	7	100.0	7	5 ABB98019	ABB98019 Zinc fing
4	7	100.0	7	5 ABB98034	ABB98034 Zinc fing
5	7	100.0	7	5 ABP49764	ABP49764 Zinc fing
6	7	100.0	7	5 ABP50067	ABP50067 Zinc fing
7	7	100.0	7	5 ABP48642	ABP48642 Zinc fing
8	7	100.0	7	5 ABP48652	ABP48652 Zinc fing
9	7	100.0	7	5 ABP49518	ABP49518 Zinc fing
10	7	100.0	7	5 ABP49797	ABP49797 Zinc fing
11	7	100.0	7	5 ABP48621	ABP48621 Zinc fing
12	7	100.0	7	5 ABP49260	ABP49260 Zinc fing
13	7	100.0	7	5 ABP50082	ABP50082 Zinc fing
14	7	100.0	7	5 ABP48649	ABP48649 Zinc fing
15	7	100.0	7	5 ABP49794	ABP49794 Zinc fing
16	7	100.0	7	5 ABP49410	ABP49410 Zinc fing
17	7	100.0	7	5 ABP49590	ABP49590 Zinc fing
18	7	100.0	7	5 ABP49515	ABP49515 Zinc fing
19	7	100.0	7	5 ABP49593	ABP49593 Zinc fing
20	7	100.0	7	5 ABP50667	ABP50667 Zinc fing
21	7	100.0	7	5 ABP49662	ABP49662 Zinc fing
22	7	100.0	7	5 ABP49902	ABP49902 Zinc fing
23	7	100.0	7	5 ABP48405	ABP48405 Zinc fing
24	7	100.0	7	5 ABP50064	ABP50064 Zinc fing
25	7	100.0	7	5 ABP50229	ABP50229 Zinc fing

26	7	100.0	7	5 ABP48216	ABP48216 Zinc fing
27	7	100.0	7	5 ABP49242	ABP49242 Zinc fing
28	7	100.0	7	5 ABP49587	ABP49587 Zinc fing
29	7	100.0	7	5 ABP49788	ABP49788 Zinc fing
30	7	100.0	7	5 ABP49791	ABP49791 Zinc fing
31	7	100.0	7	5 ABP50055	ABP50055 Zinc fing
32	7	100.0	7	5 ABP50061	ABP50061 Zinc fing
33	7	100.0	7	5 ABP50292	ABP50292 Zinc fing
34	7	100.0	7	5 ABP50058	ABP50058 Zinc fing
35	7	100.0	7	5 ABP49599	ABP49599 Zinc fing
36	7	100.0	7	5 ABP50079	ABP50079 Zinc fing
37	7	100.0	7	5 ABP49407	ABP49407 Zinc fing
38	7	100.0	7	5 ABP49701	ABP49701 Zinc fing
39	7	100.0	7	5 ABP49893	ABP49893 Zinc fing
40	7	100.0	7	5 ABP50052	ABP50052 Zinc fing
41	7	100.0	7	5 ABP48645	ABP48645 Zinc fing
42	7	100.0	7	5 ABP50085	ABP50085 Zinc fing
43	7	100.0	7	5 ABP49665	ABP49665 Zinc fing
44	7	100.0	7	5 ABP50091	ABP50091 Zinc fing
45	7	100.0	7	5 ABP50226	ABP50226 Zinc fing

ALIGNMENTS

RESULT 1
AAE08727 standard; peptide; 7 AA.
AC AAE08727;
DT 15-NOV-2001 (first entry)
DE Human KCA4 protein F1 recognition helix.
KW Human; KCA4; EPO; molecular target; zinc finger protein; ZFP;
KW cellular process; signal transduction; drug-screening.
OS Homo sapiens.
PN WO200159450-A2.
PD 16-AUG-2001.
PF 08-FEB-2001; 2001WO-US004301.
PR 08-FEB-2000; 2000US-018117P.
PA (SANG-) SANGAMO BIOSCIENCES INC.
PI Caae C;
DR WPI; 2001-522491/57.
PT Screening compound for interaction with molecular target by contacting
PT compound with cells; comprising exogenous zinc finger protein that
PT modulates expression of target, and determining values of properties of
PT cells.
PS Example 10; Page 73; 99pp; English.
XX The invention relates to a method of screening a compound for interaction
CC with a molecular target. The method involves contacting first and second
CC cells with the compound and determining the values of properties of the
CC compound. The second cell comprises an exogenous zinc finger protein
CC (ZFP) that modulates the expression of the molecular target, or isolating
CC membranes from cell comprising ZFP. The methods allow for high throughput
CC screening of candidate compound and reduces the incidence of false
CC positives. The methods are useful for screening a compound for
CC interaction with a molecular target or for screening a compound for its
CC effect on a cellular process. The method is useful for testing a compound
CC for its capacity to transduce a signal to the molecular target or its
CC capacity to block transduction of a signal through the molecular target.

CC and for performing biochemical drug-screening assays. The present
CC sequence is human Kc44 protein recognition helix used in the
CC exemplification of the invention

Sequence 7 AA; SQ

Query Match	100.0%;	Score 7;	DB 4;	Length 7;
Best Local Similarity	100.0%;	Pred. No. 1.7e+06;		
Matches 7;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	RSDHLAR	7
Db	1	RSDHLAR	7

```

RESULT 2
ABB80792
ID ABB80792 standard; peptide; 7 AA.

```

AC ABB80792;

DT 23-SEP-2002 (first entry)

DE Human ER-alpha locus targeting ZFP1 peptide #2.

KM ZFP; cytosolic; antidiabetic; ophthalmological; vasotropic; chromatin;
KM gene expression; antihypertensive; antirheumatic; antidiabetic; nootropic;
KM neuroprotective; cerebroprotective; estrogen receptor alpha; ER-alpha;
KM zinc finger protein.

OS Synthetic.

PN WO200244386-A2.

PD 06-JUN-2002.

PF 30-NOV-2001; 2001WO-US045098.

PR 01-DEC-2000; 2000US-0250804P

(SANG-) SANGAMO BIOSCIENCES INC.

PI Wolfe AP, Tse C, Collingwood T;

DR WPI: 2002-537455/57.

PT Regulating expression of gene by contacting cell with regulatory molecule
PT comprising DNA-binding domain targeted to sequence within accessible
PT region of cellular chromatin associated with a gene, and functional
PT domain.

PS Example 1; Page 44; 64pp; English

CC The invention relates to regulating the expression of a gene residing in
CC the chromatin of a cell. The method involves identifying one or more
CC accessible regions in cellular chromatin associated with gene; designing
CC a regulatory molecule, where the regulatory molecule comprises a DNA-
CC binding domain targeted to a sequence within the accessible region, and a
CC functional domain; and contacting the regulatory molecule with the cell.
CC The method is used for regulating the expression of a gene (e.g., a gene
CC encoding a nuclear receptor such as estrogen receptor alpha (ERalpha),
CC estrogen receptor beta (ERbeta), hepatocyte nuclear factor 4 alpha
CC (HNF4alpha), hepatocyte nuclear factor 1 gamma (HNF4gamma), peroxisome
CC proliferator activated receptor gamma (PPARGamma), retinoid X receptor
CC alpha (RXRalpha) or constitutively active receptor alpha (CARalpha))
CC residing in the chromatin of a cell. Regulation of gene expression (such
CC as nuclear receptor genes) will be useful in treatment of various
CC diseases, including cancer, diabetes and cardiovascular disease, where
CC the regulatory molecule as described above, is contacted with the cell to
CC carry out the regulation. The method is also useful for modulation of
CC gene expression for therapeutic or prophylactic applications e.g.,
CC diabetic retinopathy, ischaemia, macular degeneration, rheumatoid
CC arthritis, psoriasis, HIV infection, sickle cell anemia, Alzheimer's

CC disease), stroke, etc. The method also has applications in pharmaceutical
CC research of both nuclear receptors of known function as well as those of
CC unknown function. The method also facilitates development of tissue and
CC animal models of disease states, drug validation, and therapeutic product
CC development. The methods also allow identification of the role of nuclear
CC receptors of unknown functions in cellular homeostasis. Sequences
CC AB880791-817 represent zinc finger protein (ZFP) DNA-binding domains that
CC were fused to functional domains and tested for their ability to regulate
CC expression of the ER in living cells

Sequence 7 AA;

Query Match	100.0%	Score 7	DB 5	Length 7
Best Local Similarity	100.0%	Pred. No.	1.7e+06	
Matches	7	Mismatches	0	Indels 0
		Conservative	0	Gaps 0

QY	1	RSDHLAR	7
Db	1	RSDHLAR	7

RESULT 3
ABB98019
ID ABB98019 standard; peptide; 7 AA

AC ABB98019;

DT 06-SEP-2002 (first entry)

Zinc finger protein 7 finger 1 peptide

Human; heparanase; cytostatic; vasotropic; antidiabetic; anti-HIV;

KW antianaemic; neuroprotective; nootropic; cerebroprotective;

KW
cardiant; immunosuppressive; tumour metastasis; inflammatory disease;

KW extracellular matrix; cancer; ischaemia; diabetic retinopathy;

sickle cell anaemia; Alzheimer's disease; muscular dystrophy;

KW cystic fibrosis; stroke; gene therapy; zinc finger protein; ZFP.

OS Homo sapiens

PN WO200244353-A2.

PD 06-JUN-2002.

PF 30-NOV-2001; 2001WO-US044798.

PR 30-NOV-2000; 2000US-0250690P.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI WOLffe AP, Qi H;

DR WPI; 2002-527708/56

PT as tumor metastasis, inflammatory diseases and allograft rejection.

Example 3: Page 49; 72pb; English.

The invention relates to novel heparanase sequences, particularly novel sequences from the regulatory regions upstream and downstream of the coding region. The activity of polynucleotides of the invention may be described as, cytostatic, vasotropic, antidiabetic, anti-HIV, ophthalmological, antirheumatic, antiarthritic, antiproliferative, antianaemic, neuroprotective, nootropic, cerebroprotective, antibacterial, virucide, protozoacide, fungicide, antiinflammatory, cardiant and immunosuppressive. Modulating expression of heparanase gene using constructs of the invention is useful for facilitating targeted

CC control of disease states such as tumour metastasis, inflammatory
CC diseases, allograft rejection, and for inhibiting processes such as cell
CC migration, angiogenesis, and degradation of the basement membrane and/or
CC extracellular matrix. Heparanase-targeted DNA binding domains modulates
CC gene expression, and are useful for therapeutic or prophylactic
CC applications, for e.g. cancer, ischaemia, diabetic retinopathy, macular
CC degeneration, rheumatoid arthritis, psoriasis, HIV infection, sickle cell
CC anaemia, Alzheimer's disease, muscular dystrophy, neurodegenerative
CC diseases, vascular disease, cardiovascular disease, cystic fibrosis,
CC stroke, and bacterial, protozoal, fungal and viral infection. Constructs
CC of the invention may also be useful in gene therapy. The current sequence
CC represents a finger of a three-finger ZFP (zinc finger protein), which
CC has a target site in the human heparanase gene
XX
SQ Sequence 7 AA:

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7
Db 1 RSDHLAR 7

RESULT 4
ABB98034
ID ABB98034 standard; peptide; 7 AA.
XX
AC ABB98034;
XX
DT 06-SEP-2002 (first entry)
XX
DE Zinc finger protein 12 finger 1 peptide.
XX
DS
XX Human; heparanase; cytototoxic; vasotropic; antidiabetic; anti-HIV;
XX ophthalmological; antirheumatic; antiarthritic; antiproteolytic;
XX antianaemic; neuroprotective; nootropic; cerebroprotective;
XX antibacterial; virucide; protozoacide; fungicide; antiinflammatory;
XX candidant; immunosuppressive; tumour metastasis; inflammatory disease;
XX allograft rejection; cell migration; angiogenesis; basement membrane;
XX extracellular matrix; cancer; ischaemia; diabetic retinopathy;
XX macular degeneration; rheumatoid arthritis; psoriasis; HIV infection;
XX sickle cell anaemia; Alzheimer's disease; muscular dystrophy;
XX neurodegenerative disease; vascular disease; cardiovascular disease;
XX cystic fibrosis; stroke; gene therapy; zinc finger protein; ZFP.
XX
XX Homo sapiens.
XX
XX OS
XX
XX PN WO200244353-A2.
XX
XX PD 06-JUN-2002.
XX
XX PF 30-NOV-2001; 2001WO-US044798.
XX
XX PR 30-NOV-2000; 2000US-0250690P.
XX
XX PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX PI Wolffe AP, Qi H;
XX
XX DR WPI; 2002-527708/56.
XX
XX PT New heparanase polynucleotide, useful for controlling disease states such
XX as tumor metastasis, inflammatory diseases and allograft rejection.
XX
XX PS Example 3; Page 49; 72pp; English.
XX
CC The invention relates to novel heparanase sequences, particularly novel
CC sequences from the regulatory regions upstream and downstream of the
CC coding region. The activity of polynucleotides of the invention may be
CC described as, cytosstatic, vasotropic, antidiabetic, anti-HIV,
CC ophthalmological, antirheumatic, antiarthritic, antiproteolytic,

CC antianaemic, neuroprotective, nootropic, cerebroprotective,
CC antibacterial, virucide, protozoacide, fungicide, antiinflammatory,
CC cardiant and immunosuppressive. Modulating expression of heparanase gene
CC using constructs of the invention is useful for facilitating targeted
CC control of disease states such as tumour metastasis, inflammatory
CC diseases, allograft rejection, and for inhibiting processes such as cell
CC migration, angiogenesis, and degradation of the basement membrane and/or
CC extracellular matrix. Heparanase-targeted DNA binding domains modulates
CC gene expression, and are useful for therapeutic or prophylactic
CC applications, for e.g. cancer, ischaemia, diabetic retinopathy, macular
CC degeneration, rheumatoid arthritis, psoriasis, HIV infection, sickle cell
CC anaemia, Alzheimer's disease, muscular dystrophy, neurodegenerative
CC diseases, vascular disease, cardiovascular disease, cystic fibrosis,
CC stroke, and bacterial, protozoal, fungal and viral infection. Constructs
CC of the invention may also be useful in gene therapy. The current sequence
CC represents a finger of a three-finger ZFP (zinc finger protein), which
CC has a target site in the human heparanase gene
XX
SQ Sequence 7 AA:

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7
Db 1 RSDHLAR 7

RESULT 5
ABP49764
ID ABP49764 standard; peptide; 7 AA.
XX
AC ABP49764;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related peptide motif SEQ ID NO:2534.
XX
DS
XX Zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX
XX Homo sapiens.
XX
XX OS
XX Synthetic.
XX
XX PN WO200242459-A2.
XX
XX PD 30-MAY-2002.
XX
XX PF 20-NOV-2001; 2001WO-US043438.
XX
XX PR 20-NOV-2000; 2000US-00716637.
XX
XX PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX PI Liu Q;
XX
XX DR WPI; 2002-500284/53.
XX
XX PT New zinc finger protein that binds to target site, useful in studying
XX gene function and for human therapeutics and plant engineering, comprises
XX first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX PS Example 1; Page 54; 81pp; English.
XX
XX The present invention describes a zinc finger protein (I) that binds to a
XX target site, comprising a first (F1), a second (F2), and a third (F3)
XX zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
XX target site comprises, in 3'-5' direction, a first (S1), a second (S2),
XX and a third (S3) target subsite. Also described are: (1) a polypeptide
XX (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
XX (3) designing (M) (I) involves selecting the F1 zinc finger such that it
XX binds to the S1 target subsite, selecting the F2 zinc finger such that it
XX binds to the S2 target subsite, and selecting the F3 zinc finger such

CC that it binds to the S3 target subsite, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target subsites
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is
 CC useful in studying gene function, and for human therapeutics and plant
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determine the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7
 Db 1 RSDHLAR 7

RESULT 6

ABP50067
 ID ABP50067 standard; peptide; 7 AA.

XX ABP50067;

DT 28-AUG-2002 (first entry)

XX Zinc finger protein related peptide motif SEQ ID NO:2635.

KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.

OS Homo sapiens.

OS Synthetic.

PN WO200242459-A2.

XX 30-MAY-2002.

PF 20-NOV-2001; 2001WO-US043438.

XX 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

XX WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying
 PT gene function and for human therapeutics and plant engineering, comprises
 PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 56; 81bp; English.

XX The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such
 CC that it binds to the S3 target subsite, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target subsites
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is
 CC useful in studying gene function, and for human therapeutics and plant

CC engineering. (I), (II) or (III) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determine the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7
 Db 1 RSDHLAR 7

RESULT 7

ABP48642
 ID ABP48642 standard; peptide; 7 AA.

XX ABP48642;

DT 28-AUG-2002 (first entry)

XX Zinc finger protein related peptide motif SEQ ID NO:686.

KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.

OS Homo sapiens.

OS Synthetic.

PN WO200242459-A2.

XX 30-MAY-2002.

PF 20-NOV-2001; 2001WO-US043438.

XX 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

XX WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying
 PT gene function and for human therapeutics and plant engineering, comprises
 PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 41; 81bp; English.

XX The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such
 CC that it binds to the S3 target subsite, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target subsites
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is
 CC useful in studying gene function, and for human therapeutics and plant
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determine the phenotype and function of

CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention

XX Sequence 7 AA:

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RSDHLAR 7
Db 1 RSDHLAR 7

RESULT 8
ABP48652

ID ABP48652 standard; peptide; 7 AA.

XX ABP48652;

DT 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:894.

KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX Homo sapiens.

OS Synthetic.

XX WO200242459-A2.

XX 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US043438.

XX 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

WP1; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 41; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such
CC that it binds to the S3 target sub-site, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target sub-sites
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject. In
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present

CC invention
XX Sequence 7 AA:

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RSDHLAR 7
Db 1 RSDHLAR 7

RESULT 9
ABP49518

ID ABP49518 standard; peptide; 7 AA.

XX ABP49518;

DT 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:1748.

KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX Homo sapiens.

OS Synthetic.

XX WO200242459-A2.

XX 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US043438.

XX 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

WP1; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 51; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such
CC that it binds to the S3 target sub-site, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target sub-sites
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject. In
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
XX invention

XX Sequence 7 AA:

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7
Db 1 RSDHLAR 7

RESULT 10

ABP49797
ID ABP49797 standard; peptide; 7 AA.

AC ABP49797;

DT 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:2545.

KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.

OS Homo sapiens.

OS Synthetic.

PN WO200242459-A2.

PD 30-MAY-2002.

PF 20-NOV-2001; 2001WO-US043438.

PR 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

DR WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 54; 81pp; English.

CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7
Db 1 RSDHLAR 7

RESULT 11

ABP48621
ID ABP48621 standard; peptide; 7 AA.

AC ABP48621;

DT 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:679.

KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.

OS Homo sapiens.

OS Synthetic.

PN WO200242459-A2.

PD 30-MAY-2002.

PF 20-NOV-2001; 2001WO-US043438.

PR 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

DR WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 41; 81pp; English.

CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7
Db 1 RSDHLAR 7

[illegible]

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XX  Zinc finger protein related peptide motif SEQ ID NO:893.
DE  Zinc finger protein; ZFP, DNA binding protein, zinc finger.
XX
XX  Homo sapiens.
OS  Synthetic.
XX
XX  WO200242459-A2.
XX
XX  30-MAY-2002.
XX
XX  20-NOV-2001; 2001WO-US043438.
XX
XX  20-NOV-2000; 2000US-00716637.
XX
XX  (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX  Liu Q;
XX
XX  WPI; 2002-500284/53.
XX
XX  New zinc finger protein that binds to target site, useful in studying
PT  gene function and for human therapeutics and plant engineering, comprises
PT  first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX  Example 1; Page 41; 81pp; English.
XX
XX  The present invention describes a zinc finger protein (I) that binds to a
CC  target site, comprising a first (F1), a second (F2), and a third (F3)
CC  zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC  target site comprises, in 3',-5' direction, a first (S1), a second (S2),
CC  and a third (S3) target sub-site. Also described are: (I) a polypeptide
CC  (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC  (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC  binds to the S1 target sub-site, selecting the F2 zinc finger such that it
CC  binds to the S2 target sub-site, and selecting the F3 zinc finger such
CC  that it binds to the S3 target sub-site, thus designing (I) that binds to
CC  a target site. (I) is useful for recognition of triplet target sub-sites
CC  having the nucleotide G in the 5'-most position of the sub-site. (I) is
CC  useful in studying gene function, and for human therapeutics and plant
CC  engineering. (I), (II) or (III) is useful in therapeutic methods to
CC  modulate the expression of a target region within a subject, in
CC  diagnostic methods for sequence specific detection of target nucleic acid
CC  in a sample, and in assays to determined the phenotype and function of
CC  gene expression. (I) has improved affinity and specificity for their
CC  target sequences, as well as enhanced biological activity. ABQ71213 to
CC  ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC  finger peptides which are given in the exemplification of the present
CC  invention
XX
XX  Sequence 7 AA;
SQ

```

```

Query Match      100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY  1 RSDHLAR 7
    |||||
Db  1 RSDHLAR 7

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RESULT 15
ABP49794
ID  ABP49794 standard; peptide: 7 AA.
XX
XX  ABP49794;
AC
XX
XX  28-AUG-2002 (first entry)
DT
XX  Zinc finger protein related peptide motif SEQ ID NO:2544.
DE
XX  Zinc finger protein; ZFP, DNA binding protein, zinc finger.
XX
XX

```

```

XX  Homo sapiens.
OS  Synthetic.
XX
XX  WO200242459-A2.
XX
XX  30-MAY-2002.
XX
XX  20-NOV-2001; 2001WO-US043438.
XX
XX  20-NOV-2000; 2000US-00716637.
XX
XX  (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX  Liu Q;
XX
XX  WPI; 2002-500284/53.
XX
XX  New zinc finger protein that binds to target site, useful in studying
PT  gene function and for human therapeutics and plant engineering, comprises
PT  first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX  Example 1; Page 54; 81pp; English.
XX
XX  The present invention describes a zinc finger protein (I) that binds to a
CC  target site, comprising a first (F1), a second (F2), and a third (F3)
CC  zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC  target site comprises, in 3',-5' direction, a first (S1), a second (S2),
CC  and a third (S3) target sub-site. Also described are: (I) a polypeptide
CC  (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC  (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC  binds to the S1 target sub-site, selecting the F2 zinc finger such that it
CC  binds to the S2 target sub-site, and selecting the F3 zinc finger such
CC  that it binds to the S3 target sub-site, thus designing (I) that binds to
CC  a target site. (I) is useful for recognition of triplet target sub-sites
CC  having the nucleotide G in the 5'-most position of the sub-site. (I) is
CC  useful in studying gene function, and for human therapeutics and plant
CC  engineering. (I), (II) or (III) is useful in therapeutic methods to
CC  modulate the expression of a target region within a subject, in
CC  diagnostic methods for sequence specific detection of target nucleic acid
CC  in a sample, and in assays to determined the phenotype and function of
CC  gene expression. (I) has improved affinity and specificity for their
CC  target sequences, as well as enhanced biological activity. ABQ71213 to
CC  ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC  finger peptides which are given in the exemplification of the present
CC  invention
XX
XX  Sequence 7 AA;
SQ

```

```

Query Match      100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY  1 RSDHLAR 7
    |||||
Db  1 RSDHLAR 7

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Search completed: December 27, 2004, 18:06:43
Job time : 67.75 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:31 ; Search time 15.8 Seconds

(without alignments)
29.381 Million cell updates/sec

Title: US-09-846-033B-34

Perfect score: 7

Sequence: 1 RSDHLAR 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4 US-09-779-233-42	Sequence 42, Appl
2	7	100.0	100	4 US-09-248-796A-16192	Sequence 16192, A

ALIGNMENTS

RESULT 1
US-09-779-233-42
; Sequence 42, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recognition
US-09-779-233-42

Query Match 100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7
|||
DB 1 RSDHLAR 7

RESULT 2
US-09-248-796A-16192
; Sequence 16192, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16192
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16192

Query Match 100.0%; Score 7; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7
|||
DB 57 RSDHLAR 63

Search completed: December 27, 2004, 18:12:03
Job time : 15.8 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 Seconds
(without alignments)
28.393 Million cell updates/sec

Title: US-09-846-033B-99

Perfect score: 7
Sequence: 1 RSDALRQ 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	ID	Description

No matches found					

Search completed: December 27, 2004, 21:40:38
Job time : 17.35 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds
(without alignments)
29.289 Million cell updates/sec

Title: US-09-846-033B-98

Perfect score: 7
Sequence: 1 RSDALAR 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*
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5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	881	3	US-09-413-814-44 Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-09-413-814-44
; Sequence 44, Application US/09413814
; Patent No. 6225064
; GENERAL INFORMATION:
; APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
; APPLICANT: Bristol-Myers Squibb, Co.
; APPLICANT: Beyer, Stefan
; APPLICANT: Bioecker, Helmut
; APPLICANT: Brandt, Petra
; APPLICANT: Cino, Paul M
; APPLICANT: Dougherty, Brian A
; APPLICANT: Goldberg, Steven L
; APPLICANT: Hofle, Gerhard
; APPLICANT: Mueller, Joachim
; APPLICANT: Reichenbach, Hans
; TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polypeptide or
; TITLE OF INVENTION: heteropolypeptide compounds
; FILE REFERENCE: PCT/US 99/23535
; CURRENT APPLICATION NUMBER: US/09/413,814
; CURRENT FILING DATE: 1999-10-07

; EARLIER APPLICATION NUMBER: DE 198 46 493.2
; EARLIER FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 881
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-413-814-44
Query Match 100.0%; Score 7; DB 3; Length 881;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RSDALAR 7
Db 295 RSDALAR 301

Search completed: December 27, 2004, 20:31:05
Job time : 16.85 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds
(without alignments)
29.289 Million cell updates/sec

Title: US-09-846-033b-97
Perfect score: 7
Sequence: 1 QSGSLTR 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	4	US-09-731-558-16

ALIGNMENTS

RESULT 1
US-09-731-558-16
; Sequence 16, Application US/09731558
; Patent No. 6503717
; GENERAL INFORMATION:
; APPLICANT: Casey, Casey Christopher
; APPLICANT: Liu, Qiang
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
; FILE REFERENCE: 019496-003210US
; CURRENT APPLICATION NUMBER: US/09/731,558
; PRIOR APPLICATION NUMBER: US 09/456,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SBBS
; OTHER INFORMATION: recognition helix
US-09-731-558-16

Query Match 100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGSLTR 7
|||
Db 1 QSGSLTR 7

Search completed: December 27, 2004, 20:31:04
Job time : 15.85 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds
(without alignments)
29.289 Million cell updates/sec

Title: US-09-846-033B-96

Perfect score: 7
Sequence: 1 RSDALSA 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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No matches found

Search completed: December 27, 2004, 20:31:04
Job time : 15.85 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds
(without alignments)
29.289 Million cell updates/sec

Title: US-09-846-033B-95

Perfect score: 7

Sequence: 1 RSDHLTT 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 59

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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3: /cgm2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgm2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgm2_6/ptodata/1/1aa/6C_COMB.pep:*
6: /cgm2_6/ptodata/1/1aa/6D_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	US-09-614-679A-19	Sequence 19, Appl
2	7	100.0	10	US-09-139-762A-19	Sequence 19, Appl
3	7	100.0	10	US-09-139-762A-53	Sequence 53, Appl
4	7	100.0	20	US-08-040-548-19	Sequence 19, Appl
5	7	100.0	20	US-08-466-344-19	Sequence 19, Appl
6	7	100.0	21	US-09-229-007A-95	Sequence 95, Appl
7	7	100.0	21	US-10-113-424-95	Sequence 95, Appl
8	7	100.0	26	US-08-620-151-111	Sequence 111, Appl
9	7	100.0	28	US-08-040-548-34	Sequence 34, Appl
10	7	100.0	28	US-08-466-344-34	Sequence 34, Appl
11	7	100.0	28	US-09-058-459-1	Sequence 1, Appl
12	7	100.0	28	US-09-127-926-1	Sequence 1, Appl
13	7	100.0	28	US-09-037-179B-15	Sequence 15, Appl
14	7	100.0	28	US-09-240-179-2	Sequence 2, Appl
15	7	100.0	28	US-09-714-357-1	Sequence 7, Appl
16	7	100.0	28	US-09-500-700-70	Sequence 70, Appl
17	7	100.0	28	US-09-716-637-13	Sequence 13, Appl
18	7	100.0	28	US-08-040-548-7	Sequence 7, Appl
19	7	100.0	59	US-08-466-344-7	Sequence 7, Appl
20	7	100.0	85	US-09-229-007A-8	Sequence 8, Appl
21	7	100.0	85	US-10-113-424-8	Sequence 8, Appl
22	7	100.0	86	5206152-3	Patent No. 5206152
23	7	100.0	87	US-10-057-552-1	Sequence 1, Appl
24	7	100.0	89	US-08-040-548-8	Sequence 8, Appl
25	7	100.0	89	US-08-466-344-8	Sequence 8, Appl
26	7	100.0	91	US-08-863-813A-5	Sequence 5, Appl
27	7	100.0	91	US-08-676-318A-5	Sequence 5, Appl

28	7	100.0	91	US-09-500-700-5	Sequence 5, Appl
29	7	100.0	109	US-08-224-482-11	Sequence 11, Appl
30	7	100.0	153	US-08-863-813A-34	Sequence 34, Appl
31	7	100.0	153	US-08-863-813A-36	Sequence 36, Appl
32	7	100.0	153	US-08-676-318A-34	Sequence 34, Appl
33	7	100.0	153	US-08-676-318A-36	Sequence 36, Appl
34	7	100.0	153	US-09-500-700-34	Sequence 34, Appl
35	7	100.0	153	US-09-500-700-36	Sequence 36, Appl
36	7	100.0	181	US-08-863-813A-44	Sequence 44, Appl
37	7	100.0	181	US-08-676-318A-44	Sequence 44, Appl
38	7	100.0	181	US-09-500-700-44	Sequence 44, Appl
39	7	100.0	387	US-08-224-482-8	Sequence 8, Appl
40	7	100.0	387	US-09-538-092-1278	Sequence 1278, Ap
41	7	100.0	453	5206152-7	Patent No. 5206152
42	7	100.0	453	US-08-224-482-6	Sequence 6, Appl
43	7	100.0	456	US-08-040-548-2	Sequence 2, Appl
44	7	100.0	456	US-08-466-344-2	Sequence 2, Appl
45	7	100.0	456	US-09-919-039-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-09-614-679A-19
Sequence 19, Application US/09614679A
Patent No. 6492117
GENERAL INFORMATION:
APPLICANT: CHOO, YEN
APPLICANT: ISALAN, MARK
APPLICANT: BALSBRAMANTAN, SHANKAR
APPLICANT: LIU, XIAOHAI
TITLE OF INVENTION: MOLECULES
FILE REFERENCE: 71278/271599
CURRENT APPLICATION NUMBER: US/09/614, 679A
CURRENT FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-614-679A-19
Query Match 100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RSDHLTT 7
Db 1 RSDHLTT 7
RESULT 2
US-09-139-762A-19
Sequence 19, Application US/09139762A
Patent No. 6013453
GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Kluug, Aaron
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-JUN-1997
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9422534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9416880.4
FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-139-762A-19

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLLT 7
DB 1 RSDHLLT 7

RESULT 3
US-09-139-762A-53
Sequence 53, Application US/09139762A
Patent No. 6013453
GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-JUN-1997

APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9422534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9416880.4
FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-139-762A-53

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLLT 7
DB 1 RSDHLLT 7

RESULT 4
US-08-040-548-19
Sequence 19, Application US/08040548
Patent No. 5763209
GENERAL INFORMATION:
APPLICANT: Sukhame, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5763209th Clark Street, Suite 800
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/040,548
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: arcd067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-040-548-19

Query Match 100.0%; Score 7; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLLT 7
DB 9 RSDHLLT 15

RESULT 5

US-08-466-344-19
Sequence 19, Application US/08466344

Patent No. 5773583
GENERAL INFORMATION:
APPLICANT: Sukhame, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5773583th Clark Street, Suite 800
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,344
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/040,548
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: arc0067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-466-344-19

Query Match 100.0%; Score 7; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLLT 7
DB 9 RSDHLLT 15

RESULT 6

US-09-229-007A-95
Sequence 95, Application US/09229007A

Patent No. 6453242
GENERAL INFORMATION:
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Case, Casey C.
APPLICANT: Cox III, George N.
APPLICANT: Jamieson, Andrew
APPLICANT: Rebar, Edward J.
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
TITLE OF INVENTION: to Bind to Preslected Sites

FILE REFERENCE: 019496-001800US
CURRENT APPLICATION NUMBER: US/09/229,007A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 95
LENGTH: 21
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ZFP sequence
OTHER INFORMATION: (F1, F2 and F3) from Zif 268
US-09-229-007A-95

Query Match 100.0%; Score 7; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLLT 7
DB 8 RSDHLLT 14

RESULT 7

US-10-113-424-95
Sequence 95, Application US/10113424

Patent No. 6785613
GENERAL INFORMATION:
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Case, Casey C.
APPLICANT: Cox III, George N.
APPLICANT: Jamieson, Andrew
APPLICANT: Rebar, Edward J.
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
TITLE OF INVENTION: to Bind to Preslected Sites
FILE REFERENCE: 019496-001800US
CURRENT APPLICATION NUMBER: US/10/113,424
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US/09/229,007A
PRIOR FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 95
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ZFP sequence
OTHER INFORMATION: (F1, F2 and F3) from Zif 268
US-10-113-424-95

Query Match 100.0%; Score 7; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLLT 7
DB 8 RSDHLLT 14

RESULT 8

US-08-620-151-111

Sequence 111, Application US/08620151
Patent No. 5928955
GENERAL INFORMATION:
APPLICANT: Imperiali, Barbara
APPLICANT: Walkup, Grant K.
TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR
TITLE OF INVENTION: DIVALENT ZINC
NUMBER OF SEQUENCES: 136
CORRESPONDENCE ADDRESS:

ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,151
FILING DATE: 22-MAR-1996
CLASSIFICATION: 422
ATTORNEY/AGENT INFORMATION:
NAME: Shannon, Karen L.
REGISTRATION NUMBER: 36,675
REFERENCE/DOCKET NUMBER: 8597/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4239
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-620-151-111

Query Match Best Local Similarity 100.0%; Score 7; DB 2; Length 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
Db 13 RSDHLTT 19

RESULT 9
US-08-040-548-34
Sequence 34, Application US/08040548
Patent No. 5763209
GENERAL INFORMATION:
APPLICANT: Sukhame, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5763209th Clark Street, Suite 800
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/040,548
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: arc0067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961

INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-040-548-34

Query Match Best Local Similarity 100.0%; Score 7; DB 1; Length 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
Db 9 RSDHLTT 15

RESULT 10
US-08-466-344-34
Sequence 34, Application US/08466344
Patent No. 5773583
GENERAL INFORMATION:
APPLICANT: Sukhame, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5773583th Clark Street, Suite 800
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,344
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/040,548
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: arc0067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-466-344-34

Query Match Best Local Similarity 100.0%; Score 7; DB 1; Length 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
Db 9 RSDHLTT 15

RESULT 11
US-09-058-459-1

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; Sequence 1, Application US/09058459
; Patent No. 618965
; GENERAL INFORMATION:
; APPLICANT: Mayo, Stephen L.
; APPLICANT: Dahljat, Basil I.
; APPLICANT: Gordon, D. B.
; APPLICANT: Street, Arthur
; TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN
; FILE REFERENCE: A65353-3/RT/RMS/SCR
; CURRENT FILING DATE: 2000-04-10
; PRIOR FILING DATE: 1997-04-11
; PRIOR FILING DATE: 1997-04-11
; PRIOR FILING DATE: 1997-08-04
; PRIOR FILING DATE: 1997-08-04
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Mouse
US-09-058-459-1

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
Db 14 RSDHLTT 20

RESULT 12
US-09-127-926-1
; Sequence 1, Application US/09127926
; Patent No. 6269312
; GENERAL INFORMATION:
; APPLICANT: Mayo, Stephen L.
; APPLICANT: Dahljat, Basil I.
; APPLICANT: Gordon, D. Benjamin
; APPLICANT: Street, Arthur
; APPLICANT: Su, Yaoying
; TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
; FILE REFERENCE: A65353-4/RT/RMS/SCR
; CURRENT FILING DATE: 1998-07-31
; PRIOR FILING DATE: 1998-07-31
; PRIOR FILING DATE: 1997-04-11
; PRIOR FILING DATE: 1997-08-04
; PRIOR FILING DATE: 1997-08-04
; PRIOR FILING DATE: 1997-10-03
; PRIOR FILING DATE: 1997-10-03
; PRIOR FILING DATE: 1998-04-10
; PRIOR FILING DATE: 1998-04-10
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Mouse
US-09-127-926-1

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
Db 14 RSDHLTT 20

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RESULT 13
US-09-037-179B-15
; Sequence 15, Application US/09037179B
; Patent No. 616599
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; FILE REFERENCE: 0050.1312-011
; CURRENT FILING DATE: US/09/037,179B
; PRIOR FILING DATE: 1998-03-09
; PRIOR FILING DATE: 1993-08-02
; PRIOR FILING DATE: 1993-08-02
; PRIOR FILING DATE: 1990-11-13
; PRIOR FILING DATE: 1989-11-13
; PRIOR FILING DATE: 1989-11-13
; PRIOR FILING DATE: 1994-09-27
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-037-179B-15

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7
Db 17 RSDHLTT 23

RESULT 14
US-09-240-179-2
; Sequence 2, Application US/09240179
; Patent No. 6410248
; GENERAL INFORMATION:
; APPLICANT: Greisman, Harvey A.
; APPLICANT: Pabo, Carl O.
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: A General Strategy for Selecting High-Affinity Zinc
; FILE REFERENCE: 019496-000220US
; CURRENT FILING DATE: US/09/240,179
; PRIOR FILING DATE: 1999-01-29
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:24f268 zinc
; OTHER INFORMATION: finger 2
US-09-240-179-2

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Query Match 100.0%; Score 7; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLYT 7
|||
Db 13 RSDHLYT 19

RESULT 15
US-09-714-357-1

; Sequence 1, Application US/09714357
; Patent No. 6708120
; GENERAL INFORMATION:
; APPLICANT: Mayo, Stephen L.
; APPLICANT: Dahiya, Baasil I.
; APPLICANT: Gordon, D. B.
; APPLICANT: Street, Arthur
; TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN
; FILE REFERENCE: A65353-3/RPT/RMS/SJR
; CURRENT APPLICATION NUMBER: US/09/714,357
; CURRENT FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: 09/058,459
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/054,678
; PRIOR FILING DATE: 1997-08-04
; PRIOR APPLICATION NUMBER: 60/061,097
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Mouse
US-09-714-357-1

Query Match 100.0%; Score 7; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLYT 7
|||
Db 14 RSDHLYT 20

Search completed: December 27, 2004, 20:31:04
Job time : 15.85 secs